

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 09/376,317  
Source: IFW16  
Date Processed by STIC: 05/26/2006

# ***ENTERED***

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/376,317DATE: 05/26/2006  
TIME: 14:43:40

INPUT SET: S30828.raw

<p><b>This Raw Listing contains the General Information Section and up to the first 5 pages.</b></p>
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1 SEQUENCE LISTING  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: Stokes, Kenneth  
6 Morissette, Jos e  
7  
8 (ii) TITLE OF INVENTION: SYSTEM AND METHOD FOR GENETICALLY TREATING  
9 CARDIAC CONDUCTION DISTURBANCES  
10  
11 (iii) NUMBER OF SEQUENCES: 12  
12  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and Norris  
15 (B) STREET: One Liberty Place - 46th Floor  
16 (C) CITY: Philadelphia  
17 (D) STATE: PA  
18 (E) COUNTRY: U.S.A.  
19 (F) ZIP: 19103  
20  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: WordPerfect 6.1  
26  
27 (vi) CURRENT APPLICATION DATA:  
28 (A) APPLICATION NUMBER:US/09/376,317  
29 (B) FILING DATE:18-Aug-1999  
30 (C) CLASSIFICATION:  
31  
32 (vii) PRIOR APPLICATION DATA:  
33 (A) APPLICATION NUMBER:US/08/682,277  
34 (B) FILING DATE: Herewith  
35 (C) CLASSIFICATION:424  
36  
37 (viii) ATTORNEY/AGENT INFORMATION:  
38 (A) NAME: Paul K. Legaard  
39 (B) REGISTRATION NUMBER: 38,534  
40 (C) REFERENCE/DOCKET NUMBER: MEDT-0028/P-3569  
41  
42 (ix) TELECOMMUNICATION INFORMATION:  
43 (A) TELEPHONE: (215) 568-3100  
44 (B) TELEFAX: (215) 568-3439  
45  
46 (2) INFORMATION FOR SEQ ID NO:1:

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/376,317

DATE: 05/26/2006  
TIME: 14:43:41

INPUT SET: S30828.raw

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47      (i) SEQUENCE CHARACTERISTICS:
48          (A) LENGTH: 1074 bases
49          (B) TYPE: nucleic acid
50          (C) STRANDEDNESS: double
51          (D) TOPOLOGY: linear
52      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
53
54      ATG GGC GAT TGG AGC TTC CTG GGA AAT TTC CTG GAG GAA GTA CAC      45
55      Met Gly Asp Trp Ser Phe Leu Gly Asn Phe Leu Glu Glu Val His
56          1                      5                      10                      15
57
58      AAG CAC TCG ACC GTG GTA GGC AAG GTC TGG CTC ACT GTC CTC TTC      90
59      Lys His Ser Thr Val Val Gly Lys Val Trp Leu Thr Val Leu Phe
60                      20                      25                      30
61
62      ATA TTC CGT ATG CTC GTG CTG GGC ACA GCT GCT GAG TCT ACC TGG      135
63      Ile Phe Arg Met Leu Val Leu Gly Thr Ala Ala Glu Ser Thr Trp
64                      35                      40                      45
65
66      GGG GAT GAG CAG GCT GAT TTC CGG TGT GAT ACG ATT CAG CCT GGC      180
67      Gly Asp Glu Gln Ala Asp Phe Arg Cys Asp Thr Ile Gln Pro Gly
68                      50                      55                      60
69
70      TGC CAC AAT GTC TGC TAC GAC CAG GCT TTC CCC ATC TCC CAC ATT      225
71      Cys His Asn Val Cys Tyr Asp Gln Ala Phe Pro Ala Ser His Ile
72                      65                      70                      75
73
74      CGC TAC TGG GTG CTG CAG ATC ATC TTC GTC TCT ACG CCC TCT CTG      270
75      Arg Tyr Trp Val Leu Gln Ile Ile Phe Val Ser Thr Pro Ser Leu
76                      80                      85                      90
77
78      GTG TAC ATG GGC CAC GCC ATG CAC ACT GTG CGC ATG CAG GAG AAG      315
79      Val Tyr Met Gly His Ala Met His Thr Val Arg Met Gln Glu Lys
80                      95                      100                      105
81
82      CGC AAG CTA CGG GAG GCC GAG AGG GCC AAA GAG GTC CGG GGC TCT      360
83      Arg Lys Leu Arg Glu Ala Glu Arg Ala Lys Glu Val Arg Gly Ser
84                      110                      115                      120
85
86      GGC TCT TAC GAG TAC CCG GTG GCA GAG AAG GCA GAA CTG TCC TGC      405
87      Gly Ser Tyr Glu Tyr Pro Val Ala Glu Lys Ala Glu Leu Ser Cys
88                      125                      130                      135
89
90      TGG GAG GAA GGG AAT GGA AGG ATT GCC CTC CAG GGC ACT CTG CTC      450
91      Trp Glu Glu Glu Asn Gly Arg Ile Ala Leu Gln Gly Thr Leu Leu
92                      140                      145                      150
93
94      AAC ACC TAT GTG TGC AGC ATC CTG ATC CGC ACC ACC ATG GAG GTG      495
95      Asn Thr Tyr Val Cys Ser Ile Leu Ile Arg Thr Thr Met Glu Val
96                      155                      160                      165
97
98      GGC TTC ATT GTG GGC CAG TAC TTC ATC TAC GGA ATC TTC CTG ACC      540
99      Gly Phe Ile Val Gly Gln Tyr Phe Ile Tyr Gly Ile Phe Leu Thr

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/376,317

DATE: 05/26/2006  
TIME: 14:43:41

INPUT SET: S30828.raw

100		170		175		180	
101							
102	ACC CTG CAT GTC TGC CGC AGG AGT CCC TGT CCC CAC CCG GTC AAC					585	
103	Thr Leu His Val Cys Arg Arg Ser Pro Cys Pro His Pro Val Asn						
104		185		190		195	
105							
106	TGT TAC GTA TCC CGG CCC ACA GAG AAG AAT GTC TTC ATT GTC TTT					630	
107	Cys Tyr Val Ser Arg Pro Thr Glu Lys Asn Val Phe Ile Val Phe						
108		200		205		210	
109							
110	ATG CTG GCT GTG GCT GCA CTG TCC CTC CTC CTT AGC CTG GCT GAA					675	
111	Met Leu Ala Val Ala Ala Leu Ser Leu Leu Leu Ser Leu Ala Glu						
112		215		220		225	
113							
114	CTC TAC CAC CTG GGC TGG AAG AAG ATC AGA CAG CGA TTT GTC AAA					720	
115	Leu Tyr His Leu Gly Trp Lys Lys Ile Arg Gln Arg Phe Val Lys						
116		230		235		240	
117							
118	CCG CGG CAG TAC ATG GCT AAG TGC CAG CTT TCT GGC CCT CTG TGG					765	
119	Pro Arg Gln Trp Met Ala Lys Cys Gln Leu Ser Gly Pro Leu Trp						
120		245		250		255	
121							
122	GCT ATA GTC CAG AGC TGC ACA CCA CCC CCC GAC TTT AAT CAG TGC					810	
123	Ala Ile Val Gln Ser Cys Thr Pro Pro Pro Asp Phe Asn Gln Cys						
124		260		265		270	
125							
126	CTG GAG AAT GGT CCT GGG GGA AAA TTC TTC AAT CCC TTC AGC AAT					855	
127	Leu Glu Asn Gly Pro Gly Gly Lys Phe Phe Asn Pro Phe Ser Asn						
128		275		280		285	
129							
130	AAT ATG GCC TCC CAA CAA AAC ACA GAC AAC CTG GTC ACC GAG CAA					900	
131	Asn Met Ala Ser Gln Gln Asn Thr Asp Asn Leu Val Thr Glu Gln						
132		290		295		300	
133							
134	GTA CGA GGT CAG GAG CAG ACT CCT GGG GAA GGT TTC ATC CAG GTT					945	
135	Val Arg Gly Gln Glu Gln Thr Pro Gly Glu Gly Phe Ile Gln Val						
136		305		310		315	
137							
138							
139							
140							
141	CGT TAT GGC CAG AAG CCT GAG GTG CCC AAT GGA GTC TCA CCA GGT					990	
142	Arg Tyr Gly Gln Lys Pro Glu Val Pro Asn Gly Val Ser Pro Gly						
143		320		325		330	
144							
145	CAC CGC CTT CCC CAT GGC TAT CAT AGT GAC AAG CGA CGT CTT AGT					1035	
146	His Arg Leu Pro His Gly Tyr His Ser Asp Lys Arg Arg Leu Ser						
147		335		340		345	
148							
149	AAG GCC AGC AGC AAG GCA AGG TCA GAT GAC CTA TCA GTG					1074	
150	Lys Ala Ser Ser Lys Ala Arg Ser Asp Asp Leu Ser Val						
151		350		355			
152							

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/376,317

DATE: 05/26/2006  
TIME: 14:43:41

INPUT SET: S30828.raw

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153 (2) INFORMATION FOR SEQ ID NO:2:
154 (i) SEQUENCE CHARACTERISTICS:
155 (A) LENGTH: 358 amino acids
156 (B) TYPE: amino acid
157 (C) STRANDEDNESS: single
158 (D) TOPOLOGY: unknown
159 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
160
161 Met Gly Asp Trp Ser Phe Leu Gly Asn Phe Leu Glu Glu Val His
162 1 5 10 15
163
164 Lys His Ser Thr Val Val Gly Lys Val Trp Leu Thr Val Leu Phe
165 20 25 30
166
167 Ile Phe Arg Met Leu Val Leu Gly Thr Ala Ala Glu Ser Thr Trp
168 35 40 45
169
170 Gly Asp Glu Gln Ala Asp Phe Arg Cys Asp Thr Ile Gln Pro Gly
171 50 55 60
172
173 Cys His Asn Val Cys Tyr Asp Gln Ala Phe Pro Ala Ser His Ile
174 65 70 75
175
176 Arg Tyr Trp Val Leu Gln Ile Ile Phe Val Ser Thr Pro Ser Leu
177 80 85 90
178
179 Val Tyr Met Gly His Ala Met His Thr Val Arg Met Gln Glu Lys
180 95 100 105
181
182 Arg Lys Leu Arg Glu Ala Glu Arg Ala Lys Glu Val Arg Gly Ser
183 110 115 120
184
185 Gly Ser Tyr Glu Tyr Pro Val Ala Glu Lys Ala Glu Leu Ser Cys
186 125 130 135
187
188 Trp Glu Glu Glu Asn Gly Arg Ile Ala Leu Gln Gly Thr Leu Leu
189 140 145 150
190
191 Asn Thr Tyr Val Cys Ser Ile Leu Ile Arg Thr Thr Met Glu Val
192 155 160 165
193
194 Gly Phe Ile Val Gly Gln Tyr Phe Ile Tyr Gly Ile Phe Leu Thr
195 170 175 180
196
197 Thr Leu His Val Cys Arg Arg Ser Pro Cys Pro His Pro Val Asn
198 185 190 195
199
200 Cys Tyr Val Ser Arg Pro Thr Glu Lys Asn Val Phe Ile Val Phe
201 200 205 210
202
203 Met Leu Ala Val Ala Ala Leu Ser Leu Leu Leu Ser Leu Ala Glu
204 215 220 225
205

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DATE: 05/26/2006  
TIME: 14:43:41

INPUT SET: S30828.raw

206	Leu Tyr His Leu Gly Trp Lys Lys Ile Arg Gln Arg Phe Val Lys	
207		230 235 240
208		
209	Pro Arg Gln Trp Met Ala Lys Cys Gln Leu Ser Gly Pro Leu Trp	
210		245 250 255
211		
212	Ala Ile Val Gln Ser Cys Thr Pro Pro Pro Asp Phe Asn Gln Cys	
213		260 265 270
214		
215	Leu Glu Asn Gly Pro Gly Gly Lys Phe Phe Asn Pro Phe Ser Asn	
216		275 280 285
217		
218	Asn Met Ala Ser Gln Gln Asn Thr Asp Asn Leu Val Thr Glu Gln	
219		290 295 300
220		
221	Val Arg Gly Gln Glu Gln Thr Pro Gly Glu Gly Phe Ile Gln Val	
222		305 310 315
223		
224	Arg Tyr Gly Gln Lys Pro Glu Val Pro Asn Gly Val Ser Pro Gly	
225		320 325 330
226		
227	His Arg Leu Pro His Gly Tyr His Ser Asp Lys Arg Arg Leu Ser	
228		335 340 345
229		
230	Lys Ala Ser Ser Lys Ala Arg Ser Asp Asp Leu Ser Val	
231		350 355
232		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

241	ATG GGT GAC TGG AGC GCC TTA GGC AAA CTC CTT GAC AAG GTT CAA	45
242	Met Gly Asp Trp Ser Ala Leu Gly Lys Leu Leu Asp Lys Val Gln	
243	1 5 10 15	
244		
245	GCC TAC TCA ACT GCT GGA GGG AAG GTG TGG CTG TCA GTA CTT TTC	90
246	Ala Tyr Ser Thr Ala Gly Gly Lys Val Trp Leu Ser Val Leu Phe	
247	20 25 30	
248		
249	ATT TTC CGA ATC CTG CTG CTG GGG ACA GCG GTT GAG TCA GCC TGG	135
250	Ile Phe Arg Ile Leu Leu Leu Gly Thr Ala Val Glu Ser Ala Trp	
251	35 40 45	
252		
253	GGA GAT GAG CAG TCT GCC TTT CGT TGT AAC ACT CAG CAA CCT GGT	180
254	Gly Asp Glu Gln Ser Ala Phe Arg Cys Asn Thr Gln Gln Pro Gly	
255	50 55 60	
256		
257	TGT GAA AAT GTC TGC TAT GAC AAG TCT TTC CCA ATC TCT CAT GTG	225
258	Cys Glu Asn Val Cys Tyr Asp Lys Ser Phe Pro Ile Ser His Val	

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/376,317**

DATE: 05/26/2006  
TIME: 14:43:41

*INPUT SET: S30828.raw*

Line	Error	Original Text
35	Wrong Classification	(C) CLASSIFICATION:424